**BIOTECHNOLOGY
SYSTEMS
BRANCH**
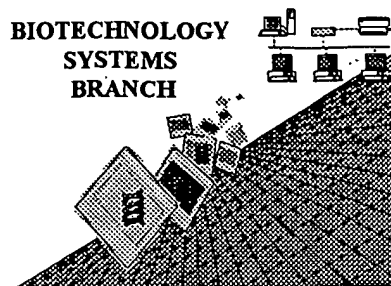
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/009,723_
Source: _Pur/lo_
Date Processed by STIC: _1/14/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
            Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, r other delivery service t : U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/009,723_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFT

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading).
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n — n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

PCT10

```
            RAW SEQUENCE LISTING              DATE: 01/14/2002
            PATENT APPLICATION:  US/10/009,723    TIME: 07:56:06  Does Not Comply
                                                            Corrected Diskette Needed

            Input Set : A:\ES.txt
            Output Set: N:\CRF3\01142002\J009723.raw


      3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
      5 <120> TITLE OF INVENTION: Diagnostic and therapeutic agents for the diseases related
monocytes and
      6       macrophages
      8 <130> FILE REFERENCE: 11214WO1
     10 <140> CURRENT APPLICATION NUMBER: US/10/009,723
     11 <141> CURRENT FILING DATE: 2001-12-17
     13 <150> PRIOR APPLICATION NUMBER: H11-171709
     14 <151> PRIOR FILING DATE: 1999-06-17
     16 <160> NUMBER OF SEQ ID NOS: 92
     18 <170> SOFTWARE: PatentIn Ver. 2.0


ERRORED SEQUENCES

    100 <210> SEQ ID NO: 3
    101 <211> LENGTH: 409
    102 <212> TYPE: DNA
    103 <213> ORGANISM: Mus musculus
    105 <220> FEATURE:
    106 <223> OTHER INFORMATION:
    108 <220> FEATURE:
    109 <221> NAME/KEY: CDS
    110 <222> LOCATION: (1)..(408)
    112 <400> SEQUENCE: 3
    113 atg gga ttc agc agg atc ttt ctc ttc ctc ctg tca gtg act aca ggt 48
    114 Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
W--> 115 -19      -15  -15   -10-              -5-0          -5
    116 gtc cac tcc cag gct ttt cta cag cag tct ggg gct gag ctg gtg agg 96
    117 Val His Ser Gln Ala Phe Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
W--> 118      -1  1      5           10
    119 cct ggg gcc tca gtg aag atg tcc tgc aag gct tct ggc tac aca ttt 144
    120 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
W--> 121      15      20      25
    122 atc aat tac aat atg cac tgg gta aag cag aca cct aga cag ggc ctg 192
    123 Ile Asn Tyr Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu
W--> 124 30      35      40      45
    125 gaa tgg att gga gct att ttt cca gga aat ggt ttt act tcc tac aat 240
    126 Glu Trp Ile Gly Ala Ile Phe Pro Gly Asn Gly Phe Thr Ser Tyr Asn
W--> 127      50      55      60
    128 cag aag ttc aag ggc aag gcc aca ctg act gta gac aaa tcc tcc agc 288
    129 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
W--> 130      65      70      75
    131 aca gtc tac atg cag ctc cgc agc ctg aca tct gaa gac tct gcg gtc 336
E--> 132 Thr Val Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val  80
E--> 133 85              90
    134 tat ttc tgt gca aga gat ggt gac tat tac ttt gac tac tgg ggc caa 384
    135 Tyr Phe Cys Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr Trp Gly Gln
```

(global error)

misaligned amino acid numbers

(see item 3 on Error Summary sheet)

insert a hard return

initial letter of amino acid is always in upper-case letter

same error

same

same

same

misaligned

```
                RAW SEQUENCE LISTING            DATE: 01/14/2002
                PATENT APPLICATION:  US/10/009,723   TIME: 07:56:07

                      Input Set : A:\ES.txt
                      Output Set: N:\CRF3\01142002\J009723.raw

W--> 136    95          100          105    misaligned
E--> 137 ggc acc act ctc aca gtc tcc tca g              409
     138 Gly Thr Thr Leu Thr Val Ser Ser
E--> 139 110        115      117   misaligned
     179 <210> SEQ ID NO: 5                    Per 1.822 of Sequence
     180 <211> LENGTH: 5                       Rules, number the
     181 <212> TYPE: PRT                       amino acids under
     182 <213> ORGANISM: Mus musculus          every 5 amino
     184 <220> FEATURE:                        acids
     185 <223> OTHER INFORMATION:              (global err)
     187 <400> SEQUENCE: 5
     188 Ser Asn Tyr Ile Ser     misaligned
E--> 189 1      5       5
     191 <210> SEQ ID NO: 6
     192 <211> LENGTH: 17
     193 <212> TYPE: PRT
     194 <213> ORGANISM: Mus musculus
     196 <220> FEATURE:
     197 <223> OTHER INFORMATION:
     199 <400> SEQUENCE: 6
     200 Trp Ile Tyr Ala Gly Thr Gly Asp Ala Ser Tyr Asn Gln Lys Phe Thr
E--> 201 1         5          10          15
     202 Ala
     203 17
     205 <210> SEQ ID NO: 7
     206 <211> LENGTH: 10
     207 <212> TYPE: PRT
     208 <213> ORGANISM: Mus musculus
     210 <220> FEATURE:
     211 <223> OTHER INFORMATION:
     213 <400> SEQUENCE: 7
     214 His Gly Gly Asp Gly Tyr Trp Phe Ala Tyr
E--> 215 1         5          10                 same
     217 <210> SEQ ID NO: 8
     218 <211> LENGTH: 10
     219 <212> TYPE: PRT
     220 <213> ORGANISM: Mus musculus
     222 <220> FEATURE:
     223 <223> OTHER INFORMATION:
     225 <400> SEQUENCE: 8
     226 Ser Ala Ser Ser Ser Val Ser Tyr Met His
E--> 227 1         5          10
     229 <210> SEQ ID NO: 9
     230 <211> LENGTH: 7
     231 <212> TYPE: PRT
     232 <213> ORGANISM: Mus musculus
     234 <220> FEATURE:
     235 <223> OTHER INFORMATION:
     237 <400> SEQUENCE: 9
```

Input Set : A:\ES.txt
Output Set: N:\CRF3\01142002\J009723.raw

```
       238 Asp Thr Ser Lys Leu Pro Ser          number amend acids render every 5
E--> 239 1        5          7                              amend
       241 <210> SEQ ID NO: 10                              acids
       242 <211> LENGTH: 9
       243 <212> TYPE: PRT
       244 <213> ORGANISM: Mus musculus
       246 <220> FEATURE:
       247 <223> OTHER INFORMATION:
       249 <400> SEQUENCE: 10
       250 Gln Gln Trp Ser Ser Asn Pro Pro Thr
E--> 251 1        5                 9
       253 <210> SEQ ID NO: 11
       254 <211> LENGTH: 5
       255 <212> TYPE: PRT
       256 <213> ORGANISM: Mus musculus               same
       258 <220> FEATURE:
       259 <223> OTHER INFORMATION:
       261 <400> SEQUENCE: 11
       262 Asn Tyr Asn Met His
E--> 263 1        5
       265 <210> SEQ ID NO: 12
       266 <211> LENGTH: 17
       267 <212> TYPE: PRT
       268 <213> ORGANISM: Mus musculus
       270 <220> FEATURE:
       271 <223> OTHER INFORMATION:
       273 <400> SEQUENCE: 12
       274 Ala Ile Phe Pro Gly Asn Gly Phe Thr Ser Tyr Asn Gln Lys Phe Lys
E--> 275 1        5          10          15
       276 Gly
       277 17
       279 <210> SEQ ID NO: 13
       280 <211> LENGTH: 8
       281 <212> TYPE: PRT
       282 <213> ORGANISM: Mus musculus
       284 <220> FEATURE:
       285 <223> OTHER INFORMATION:
       287 <400> SEQUENCE: 13
       288 Asp Gly Asp Tyr Tyr Phe Asp Tyr
E--> 289 1        5              8
       291 <210> SEQ ID NO: 14
       292 <211> LENGTH: 10
       293 <212> TYPE: PRT
       294 <213> ORGANISM: Mus musculus
       296 <220> FEATURE:
       297 <223> OTHER INFORMATION:
       299 <400> SEQUENCE: 14
       300 Ser Ala Ser Ser Ser Val Ser Tyr Met His
E--> 301 1        5          10
```

RAW SEQUENCE LISTING   DATE: 01/14/2002
PATENT APPLICATION: US/10/009,723   TIME: 07:56:07

Input Set : A:\ES.txt
Output Set: N:\CRF3\01142002\J009723.raw

```
      303 <210> SEQ ID NO: 15
      304 <211> LENGTH: 7
      305 <212> TYPE: PRT
      306 <213> ORGANISM: Mus musculus
      308 <220> FEATURE:
      309 <223> OTHER INFORMATION:
      311 <400> SEQUENCE: 15
      312 Arg Thr Ser Asn Leu Ala Ser
E--> 313 1         5        7          same
      315 <210> SEQ ID NO: 16
      316 <211> LENGTH: 7
      317 <212> TYPE: PRT
      318 <213> ORGANISM: Mus musculus
      320 <220> FEATURE:
      321 <223> OTHER INFORMATION:
      323 <400> SEQUENCE: 16
      324 His Gln Trp Ser Met Tyr Thr
E--> 325 1         5        7          same
E--> 394 <210> SEQ ID NO: 22  23
      395 <211> LENGTH: 33
      396 <212> TYPE: DNA
      397 <213> ORGANISM: Artificial Sequence
      399 <220> FEATURE:
      400 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
E--> 402 <400> SEQUENCE: 23
      403 cgttcggagg ggggaccaag ctggaaataa aac                                    33
E--> 405 <210> SEQ ID NO: 24   ignore - this is due to above error
      488 <210> SEQ ID NO: 31
      489 <211> LENGTH: 421  4/5 (p.5)
      490 <212> TYPE: DNA
      491 <213> ORGANISM: Artificial Sequence
      493 <220> FEATURE:
      494 <223> OTHER INFORMATION: Description of Artificial Sequence:Synthetic DNA
      496 <220> FEATURE:
      497 <221> NAME/KEY: CDS
      498 <222> LOCATION: (1)..(420)
      500 <400> SEQUENCE: 31
      501 atg gaa tgg aac tgg gtc gtt ctc ttc ctc ctg tca tta act gca ggt 48
      502 Met Glu Trp Asn Trp Val Val Leu Phe Leu Leu Ser Leu Thr Ala Gly
W--> 503 -19      -15      -10      -5
      504 gtc tat gcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96
      505 Val Tyr Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
W--> 506     -1 1      5        10
      507 cct ggc gcc tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc 144
      508 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
W--> 509     15       20       25
      510 agc agt aac tat ata agt tgg gtg cga cag gcc cct gga caa ggg ctt 192
      511 Ser Ser Asn Tyr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
W--> 512 30       35       40          45
```

misaligned
hos.

RAW SEQUENCE LISTING   DATE: 01/14/2002
PATENT APPLICATION: US/10/009,723   TIME: 07:56:07

Input Set : A:\ES.txt
Output Set: N:\CRF3\01142002\J009723.raw

```
      513 gag tgg atg gga tgg att tat gct gga act ggt gat gcc agc tat aat 240
      514 Glu Trp Met Gly Trp Ile Tyr Ala Gly Thr Gly Asp Ala Ser Tyr Asn
W--> 515       50        55        60
      516 cag aag ttc aca gcc aga gtc acc att acc gtc gac aca tcc acg agc 288
      517 Gln Lys Phe Thr Ala Arg Val Thr Ile Thr Val Asp Thr Ser Thr Ser
W--> 518       65        70        75
      519 aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 336
      520 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
W--> 521       80        85        90
      522 tat tac tgt gcg aga cac ggg ggg gac ggc tac tgg ttt gct tac tgg 384
      523 Tyr Tyr Cys Ala Arg His Gly Gly Asp Gly Tyr Trp Phe Ala Tyr Trp
W--> 524       95        100        105
      525 ggc cag gga acc ctg gtc acc gtc tcc tca g               415
      526 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
E--> 527      110        115
      642 <210> SEQ ID NO: 39
      643 <211> LENGTH: 87
      644 <212> TYPE: DNA
      645 <213> ORGANISM: Artificial Sequence
      647 <220> FEATURE:
      648 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
      650 <400> SEQUENCE: 39
W--> 651 caggaaacag ctatgacgaa ttccaccatg gattttcaag tgcagatttt cagcttcctg 60ctaatcagtg
     652 cctcagtcat aatatcc                                       87
      654 <210> SEQ ID NO: 40
      655 <211> LENGTH: 93
      656 <212> TYPE: DNA
      657 <213> ORGANISM: Artificial Sequence
      659 <220> FEATURE:
      660 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
      662 <400> SEQUENCE: 40aagtgatggt gactctgtct cctacagatg cagacaggga ggatggagac tgggtcatct
E--> 663 ggatatctcc tctggatatt atgactgagg cac                     93
      974 <210> SEQ ID NO: 63
      975 <211> LENGTH: 8
      976 <212> TYPE: DNA
      977 <213> ORGANISM: Artificial Sequence
      979 <220> FEATURE:
      980 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
      982 <400> SEQUENCE: 63
      983 agacagagtc accatcactt gtagtgccag ctcgagtgta agttacatgc actggtatca  60
E--> 984 gcagaaacca gggaaagccc ctaag                              85
     1282 <210> SEQ ID NO: 82
     1283 <211> LENGTH: 138
     1284 <212> TYPE: PRT
     1285 <213> ORGANISM: Mus musculus
     1287 <220> FEATURE:
     1288 <223> OTHER INFORMATION:
     1290 <400> SEQUENCE: 82
     1291 Met Glu Trp Asn Trp Val Val Leu Phe Leu Leu Ser Leu Thr Ala Gly
```

```
              RAW SEQUENCE LISTING              DATE: 01/14/2002
              PATENT APPLICATION:  US/10/009,723   TIME: 07:56:07

                     Input Set : A:\ES.txt
                     Output Set: N:\CRF3\01142002\J009723.raw


      1292 -19              -15                -10                -5
      1293 Val Tyr Ala Gln Gly Gln Met Gln Gln Ser Gly Ala Glu Leu Val Lys
E--> 1294     -1 1       5         10
      1295 Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Pro Ser Gly Phe Thr Phe
E--> 1296     15        20        25
      1297 Ser Ser Asn Tyr Ile Ser Trp Leu Lys Gln Lys Pro Gly Gln Ser Leu
E--> 1298     30        35        40        45
      1299 Glu Trp Ile Ala Trp Ile Tyr Ala Gly Thr Gly Asp Ala Ser Tyr Asn
E--> 1300        50        55        60
      1301 Gln Lys Phe Thr Ala Lys Ala His Val Thr Val Asp Thr Ser Ser Ser
E--> 1302     65        70        75
      1303 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Thr Glu Asp Ser Ala Ile
E--> 1304     80        85        90
      1305 Tyr Tyr Cys Ala Arg His Gly Gly Asp Gly Tyr Trp Phe Ala Tyr Trp
E--> 1306     95        100        105
      1307 Gly Gln Gly Thr Leu Val Thr Val Ser Ala
E--> 1308 110       115        119
      1310 <210> SEQ ID NO: 83
      1311 <211> LENGTH: 128
      1312 <212> TYPE: PRT
      1313 <213> ORGANISM: Mus musculus
      1315 <220> FEATURE:
      1316 <223> OTHER INFORMATION:
      1318 <400> SEQUENCE: 83
      1319 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
E--> 1320 -22  -20        -15        -10
      1321 Val Ile Ile Ser Arg Gly Gln Leu Val Leu Thr Gln Ser Pro Ala Ile
E--> 1322     -5        -1 1       5         10
      1323 Met Ser Ala Ser Gln Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser
E--> 1324        15        20        25
      1325 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
E--> 1326        30        35        40
      1327 Pro Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Pro Ser Gly Val Pro
E--> 1328     45        50        55
      1329 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
E--> 1330     60        65        70
      1331 Ser Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
E--> 1332     75        80        85        90
      1333 Ser Ser Asn Pro Pro Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
E--> 1334        95        100        105 106
      1336 <210> SEQ ID NO: 84
      1337 <211> LENGTH: 136
      1338 <212> TYPE: PRT
      1339 <213> ORGANISM: Mus musculus
      1341 <220> FEATURE:
      1342 <223> OTHER INFORMATION:
      1344 <400> SEQUENCE: 84
      1345 Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
E--> 1346 -19              -15        -10        -5
```

misaligned nos.

same error

same

```
        1347 Val His Ser Gln Ala Phe Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
E--> 1348       -1  1          5           10
        1349 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
E--> 1350       15          20          25
        1351 Ile Asn Tyr Asn Met His Trp Val Lys Gln Thr Pro Arg Gln Gly Leu
E--> 1352 30          35          40          45
        1353 Glu Trp Ile Gly Ala Ile Phe Pro Gly Asn Gly Phe Thr Ser Tyr Asn
E--> 1354       50          55          60
        1355 Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser
E--> 1356       65          70          75
        1357 Thr Val Tyr Met Gln Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val
E--> 1358       80          85          90
        1359 Tyr Phe Cys Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr Trp Gly Gln
E--> 1360       95          100         105
        1361 Gly Thr Thr Leu Thr Val Ser Ser
E--> 1362 110         115       (117)
        1364 <210> SEQ ID NO: 85
        1365 <211> LENGTH: 126
        1366 <212> TYPE: PRT
        1367 <213> ORGANISM: Mus musculus
        1369 <220> FEATURE:
        1370 <223> OTHER INFORMATION:
        1372 <400> SEQUENCE: 85
        1373 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
E--> 1374 -22  -20        -15         -10
        1375 Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
E--> 1376    -5         -1  1         5           10
        1377 Met Ser Ala Ser Leu Gly Glu Glu Ile Thr Leu Thr Cys Ser Ala Ser
E--> 1378       15          20          25
        1379 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Ser Gly Thr Ser
E--> 1380       30          35          40
        1381 Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro
E--> 1382       45          50          55
        1383 Phe Arg Phe Ser Gly Ser Gly Ser Gly Thr Phe Tyr Ser Leu Thr Ile
E--> 1384 60          65          70
        1385 Ser Ser Val Glu Ala Glu Asp Ala Ala Asp Tyr Tyr Cys His Gln Trp
E--> 1386 75          80          85          90
        1387 Ser Met Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
E--> 1388       95          100        (104)
        1390 <210> SEQ ID NO: 86
        1391 <211> LENGTH: (140)
        1392 <212> TYPE: PRT
        1393 <213> ORGANISM: Artificial Sequence
        1395 <220> FEATURE:
        1396 <223> OTHER INFORMATION: Description of Artificial Sequence: Humanized antibody
        1398 <400> SEQUENCE: 86
        1399 Met Glu Trp Asn Trp Val Val Leu Phe Leu Leu Ser Leu Thr Ala Gly
E--> 1400 -19         -15         -10         -5
        1401 Val Tyr Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
```

same

same

138(p. 8)   number the amino acids under every 5 amino acids

same

RAW SEQUENCE LISTING   DATE: 01/14/2002
PATENT APPLICATION: US/10/009,723   TIME: 07:56:07

Input Set : A:\ES.txt
Output Set: N:\CRF3\01142002\J009723.raw

```
E--> 1402      -1  1       5          10
     1403 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
E--> 1404    15        20        25
     1405 Ser Ser Asn Tyr Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
E--> 1406 30       35       40          45
     1407 Glu Trp Met Gly Trp Ile Tyr Ala Gly Thr Gly Asp Ala Ser Tyr Asn
E--> 1408        50       55       60
     1409 Gln Lys Phe Thr Ala Arg Val Thr Ile Thr Val Asp Thr Ser Thr Ser     same
E--> 1410      65       70       75
     1411 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
E--> 1412      80       85       90
     1413 Tyr Tyr Cys Ala Arg His Gly Gly Asp Gly Tyr Trp Phe Ala Tyr Trp
E--> 1414      95       100      105
     1415 Gly Gln Gly Thr Leu Val Thr Val Ser Ser
E--> 1416 110      115       119
     1418 <210> SEQ ID NO: 87
     1419 <211> LENGTH: 136
     1420 <212> TYPE: PRT
     1421 <213> ORGANISM: Artificial Sequence
     1423 <220> FEATURE:
     1424 <223> OTHER INFORMATION: Description of Artificial Sequence: Humanized antibody
     1426 <400> SEQUENCE: 87
     1427 Met Gly Phe Ser Arg Ile Phe Leu Phe Leu Leu Ser Val Thr Thr Gly
     1428 -19          -15               -10                -5
     1429 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
     1430         -1  1        5              10
     1431 Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
     1432      15             20             25
     1433 Ile Asn Tyr Asn Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
     1434 30             35             40               45
     1435 Glu Trp Met Gly Ala Ile Phe Pro Gly Asn Gly Phe Thr Ser Tyr Asn
     1436              50             55             60
     1437 Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Val Asp Lys Ser Thr Ser
     1438         65             70             75
     1439 Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
     1440      80             85             90
     1441 Tyr Tyr Cys Ala Arg Asp Gly Asp Tyr Tyr Phe Asp Tyr Trp Gly Gln     insert
E--> 1442 100           105                                             95    hard
     1443 Gly Thr Leu Val Thr Val Ser Ser                                     return
E--> 1444 110           115       117
     1446 <210> SEQ ID NO: 88
     1447 <211> LENGTH: 128
     1448 <212> TYPE: PRT
     1449 <213> ORGANISM: Artificial Sequence
     1451 <220> FEATURE:
     1452 <223> OTHER INFORMATION: Description of Artificial Sequence: Humanized antibody
     1454 <400> SEQUENCE: 88
     1455 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
E--> 1456 -22   -20         -15         -10    misaligned nos.
```

```
       1457 Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
E-->   1458    -5          -1  1          5          10
       1459 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
E-->   1460        15          20          25
       1461 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
E-->   1462        30          35          40
       1463 Pro Lys Leu Leu Ile Tyr Asp Thr Ser Lys Leu Pro Ser Gly Val Pro
E-->   1464        45          50          55
       1465 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
E-->   1466        60          65          70
       1467 Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Trp
E-->   1468    75          80          85          90
       1469 Ser Ser Asn Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
E-->   1470        95          100         105 (106)
       1498 <210> SEQ ID NO: 90
       1499 <211> LENGTH: 126
       1500 <212> TYPE: PRT
       1501 <213> ORGANISM: Artificial Sequence
       1503 <220> FEATURE:
       1504 <223> OTHER INFORMATION: Description of Artificial Sequence: Humanized antibody
       1506 <400> SEQUENCE: 90
       1507 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
       1508 -22      -20                 -15                 -10
       1509 Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
       1510    -5              -1  1          5                      10
       1511 Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Ser Ala Ser
       1512            15              20              25
       1513 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
E-->   1514            30                  35              40 Pro Lys Leu Leu Ile Tyr
E-->   1515 Arg Thr Ser Asn Leu Ala Ser Gly Val Pro
E-->   1516            45              50                  55
       1517 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
E-->   1518        60              65              70
       1519 Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Trp
E-->   1520    75              80              85                  90
       1521 Ser Met Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
E-->   1522                95                  100     (104)
       1552 <210> SEQ ID NO: 92
       1553 <211> LENGTH: 126
       1554 <212> TYPE: PRT
       1555 <213> ORGANISM: Artificial Sequence
       1557 <220> FEATURE:
       1558 <223> OTHER INFORMATION: Description of Artificial Sequence: Humanized antibody
       1560 <400> SEQUENCE: 92
       1561 Met Asp Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
       1562 -22      -20                 -15                 -10
       1563 Val Ile Ile Ser Arg Gly Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
       1564    -5              -1  1          5                      10
       1565 Leu Ser Ala Ser Val Gly Glu Glu Val Thr Ile Thr Cys Ser Ala Ser
```

misaligned nos.

delete - number the amino acids under every 5 amino acids

insert hard return

delete

P. 10

RAW SEQUENCE LISTING   DATE: 01/14/2002
PATENT APPLICATION: US/10/009,723   TIME: 07:56:07

Input Set : A:\ES.txt
Output Set: N:\CRF3\01142002\J009723.raw

```
1566              15              20              25
1567 Ser Ser Val Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Lys Ala
1568          30              35              40
1569 Pro Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro
1570      45              50              55
1571 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Phe Tyr Thr Leu Thr Ile
1572          60              65              70  70
1573 Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys His Gln Trp
1574 75              80              85              90
1575 Ser Met Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
1576              95              100
```

E--> 1572 ← *fix this*

70 70

104 delete

see next page for more error

insert a hard return

<210> 52
<211> 379<212> DNA
<213> Artificial Sequence

same erra in Seq. 78

FYI Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01142002\J009723.raw**

```
L:10  M:270 C: Current Application Number differs, Replaced Application Number
L:11  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:38  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:41  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:44  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:47  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:50  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:53  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:56  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:59  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:76  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:79  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:82  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:85  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:88  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:91  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:94  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:97  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:132 M:254 E: No. of Bases conflict, LENGTH:Input:80 Counted:384 SEQ:3
L:132 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:14
L:132 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=3
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:139 M:252 E: No. of Seq. differs, <211>LENGTH:Input:409 Found:457 SEQ:3
L:156 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:168 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:189 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:201 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
L:215 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7
L:227 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:239 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:251 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:263 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
```

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01142002\J009723.raw**

```
L:275  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
L:289  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:13
L:301  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:313  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:15
L:325  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
L:394  M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO:22
L:402  M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:23
L:405  M:214 E: (33) Seq.# missing, SEQ ID NO:23
L:503  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:506  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:509  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:512  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:515  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:518  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:521  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:524  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:527  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:31
L:527  M:252 E: No. of Seq. differs, <211>LENGTH:Input:421 Found:415 SEQ:31
L:651  M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:7
L:652  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:39
L:652  M:254 E: No. of Bases conflict, LENGTH:Input:87 Counted:17 SEQ:39
L:652  M:252 E: No. of Seq. differs, <211>LENGTH:Input:87 Found:17 SEQ:39
L:663  M:254 E: No. of Bases conflict, LENGTH:Input:93 Counted:33 SEQ:40
L:663  M:252 E: No. of Seq. differs, <211>LENGTH:Input:93 Found:33 SEQ:40
L:728  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:731  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:734  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:737  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:740  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:743  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:746  M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:45
L:835  M:282 W: Numeric Field Identifier Missing, <212> is required.
L:904  M:112 C: (48) String data converted to lower case,
L:984  M:252 E: No. of Seq. differs, <211>LENGTH:Input:8 Found:85 SEQ:63
L:1216 M:282 W: Numeric Field Identifier Missing, <212> is required.
L:1294 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:82
M:332 Repeated in SeqNo=82
L:1320 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:83
M:332 Repeated in SeqNo=83
L:1346 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:84
M:332 Repeated in SeqNo=84
L:1374 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:85
M:332 Repeated in SeqNo=85
L:1400 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:86
M:332 Repeated in SeqNo=86
L:1416 M:252 E: No. of Seq. differs, <211>LENGTH:Input:140 Found:138 SEQ:86
L:1442 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:87
M:332 Repeated in SeqNo=87
L:1444 M:252 E: No. of Seq. differs, <211>LENGTH:Input:136 Found:120 SEQ:87
```

Input Set : **A:\ES.txt**
Output Set: **N:\CRF3\01142002\J009723.raw**

L:1456 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:88
M:332 Repeated in SeqNo=88
L:1514 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:90
L:1514 M:333 E: Wrong sequence grouping, Amino acids not in groups!
M:332 Repeated in SeqNo=90
L:1522 M:252 E: No. of Seq. differs, <211>LENGTH:Input:126 Found:125 SEQ:90
L:1572 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:92